



078-us1.ST25  
SEQUENCE LISTING

<110> Paz Einat, Louis Deiss, and Ruth Maya  
<120> ISOCITRATE DEHYDROGENASE AND USES THEREOF  
<130> 67723-A; 078-US1  
<140>  
<141>  
<150> 60/395364  
<151> 2002-07-11  
<160> 6  
<170> PatentIn version 3.2  
<210> 1  
<211> 2301  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (247)..(1491)

<400> 1  
ggcggcgaag cgggggcacg ccctcgaca cgcagagata aattgtgctc ccatgacctt 60  
tatttggaag gtgcctgcgg gcctaaatt ggcctttgtc ccaccgagta cactcagcac 120  
tgtactttaa accggataaa ctgggctgtc tggcaggcga taaactacat tcagttgagt 180  
ctgcaagact gggaggaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa 240  
gtcaaa atg tcc aaa aaa atc agt ggc ggt tct gtg gta gag atg caa 288  
Met Ser Lys Lys Ile Ser Gly Gly Ser Val Val Glu Met Gln  
1 5 10  
gga gat gaa atg aca cga atc att tgg gaa ttg att aaa gag aaa ctc 336  
Gly Asp Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu  
15 20 25 30  
att ttt ccc tac gtg gaa ttg gat cta cat agc tat gat tta ggc ata 384  
Ile Phe Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile  
35 40 45  
gag aat cgt gat gcc acc aac gac caa gtc acc aag gat gct gca gaa 432  
Glu Asn Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu  
50 55 60  
gct ata aag aag cat aat gtt ggc gtc aaa tgt gcc act atc act cct 480  
Ala Ile Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro  
65 70 75  
gat gag aag agg gtt gag gag ttc aag ttg aaa caa atg tgg aaa tca 528  
Asp Glu Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser  
80 85 90  
cca aat ggc acc ata cga aat att ctg ggt ggc acg gtc ttc aga gaa 576  
Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu

Page 1

95	078-us1.ST25										110	
	100										105	
gcc att atc tgc aaa aat atc ccc cgg ctt gtg agt gga tgg gta aaa	624											
Ala Ile Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys												
	115											
cct atc atc ata ggt cgt cat gct tat ggg gat caa tac aga gca act	672											
Pro Ile Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr												
	130											
gat ttt gtt gtt cct ggg cct gga aaa gta gag ata acc tac aca cca	720											
Asp Phe Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro												
	145											
agt gac gga acc caa aag gtg aca tac ctg gta cat aac ttt gaa gaa	768											
Ser Asp Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu												
	160											
ggg ggt ggt gtt gcc atg ggg atg tat aat caa gat aag tca att gaa	816											
Gly Gly Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu												
	175											
gat ttt gca cac agt tcc ttc caa atg gct ctg tct aag ggt tgg cct	864											
Asp Phe Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro												
	195											
ttg tat ctg agc acc aaa aac act att ctg aag aaa tat gat ggg cgt	912											
Leu Tyr Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg												
	210											
ttt aaa gac atc ttt cag gag ata tat gac aag cag tac aag tcc cag	960											
Phe Lys Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln												
	225											
ttt gaa gct caa aag atc tgg tat gag cat agg ctc atc gac gac atg	1008											
Phe Glu Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met												
	240											
gtg gcc caa gct atg aaa tca gag gga ggc ttc atc tgg gcc tgt aaa	1056											
Val Ala Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys												
	255											
aac tat gat ggt gac gtg cag tgc gag tct gtg gcc caa ggg tat ggc	1104											
Asn Tyr Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly												
	275											
tct ctc ggc atg atg acc agc gtg ctg gtt tgt cca gat ggc aag aca	1152											
Ser Leu Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr												
	290											
gta gaa gca gag gct gcc cac ggg act gta acc cgt cac tac cgc atg	1200											
Val Glu Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met												
	305											
tac cag aaa gga cag gag acg tcc acc aat ccc att gct tcc att ttt	1248											
Tyr Gln Lys Gly Gln Glu Thr Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe												
	320											
gcc tgg acc aga ggg tta gcc cac aga gca aag ctt gat aac aat aaa	1296											
Ala Trp Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys												
	335											
	340											
	345											
	350											

078-us1.ST25

gag ctt gcc ttc ttt gca aat gct ttg gaa gaa gtc tct att gag aca	1344
Glu Leu Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr	
	355
	360
	365
att gag gct ggc ttc atg acc aag gac ttg gct gct tgc att aaa ggt	1392
Ile Glu Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly	
	370
	375
	380
tta ccc aat gtg caa cgt tct gac tac ttg aat aca ttt gag ttc atg	1440
Leu Pro Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met	
	385
	390
	395
gat aaa ctt gga gaa aac ttg aag atc aaa cta gct cag gcc aaa ctt	1488
Asp Lys Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu	
	400
	405
	410
tta gttcatacct gagctaagaa ggataattgt ctttttggttaa ctaggtctac	1541
aggttttacat ttttctgtgt tacactcaag gataaaggca aaatcaattt tgtaatttgt	1601
ttagaagcca gagtttatct tttctataag ttacagcct ttttcttata tatacagtta	1661
ttgccacctt tgtgaacatg gcaagggact tttttacaat ttttatttta ttttctagta	1721
ccagcctagg aattcggtta gtactcattt gtattcactg tcactttttc tcatgttcta	1781
attataaatg accaaaatca agattgctca aaagggtaaa tgatagccac agtattgctc	1841
cctaaaatat gcataaagta gaaattcact gccttcccct cctgtccatg accttgggca	1901
caggaagtt ctggtgtcat agatatcccg ttttgtgagg tagagctgtg cattaaactt	1961
gcacatgact ggaacgaagt aggagtgc aaatcaatgtg ttgaagatac tgcagtcatt	2021
tttgtaaaga ccttgctgaa tgtttccaat agactaaata ctgttttaggc cgcaggagag	2081
tttggaatcc ggaataaata ctacctggag gtttgtcctc tccatttttc tctttctcct	2141
cctggcctgg cctgaatatt atactactct aaatagcata tttcatccaa gtgcaataat	2201
gtaagctgaa tcttttttgg acttctgctg gcctgtttta tttcttttat ataaatgtga	2261
tttctcagaa attgatatta aacactatct tatcttctcc	2301

<210> 2  
 <211> 414  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Ser Lys Lys Ile Ser Gly Gly Ser Val Val Glu Met Gln Gly Asp  
 1 5 10 15

Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu Ile Phe  
 20 25 30

Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn  
 35 40 45

## 078-us1.ST25

Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile  
 50 55 60  
 Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu  
 65 70 75 80  
 Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn  
 85 90 95  
 Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile  
 100 105 110  
 Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys Pro Ile  
 115 120 125  
 Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr Asp Phe  
 130 135 140  
 Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp  
 145 150 155 160  
 Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly  
 165 170 175  
 Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe  
 180 185 190  
 Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr  
 195 200 205  
 Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys  
 210 215 220  
 Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu  
 225 230 235 240  
 Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala  
 245 250 255  
 Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr  
 260 265 270  
 Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu  
 275 280 285  
 Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu  
 290 295 300

078-us1.ST25

Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln  
305 310 315 320

Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp  
325 330 335

Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu  
340 345 350

Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu  
355 360 365

Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro  
370 375 380

Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys  
385 390 395 400

Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu  
405 410

<210> 3  
<211> 1740  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (87)..(1445)

<400> 3  
ccagcggttag cccgcggcca ggcagccggg aggagcggcg cgcgctcgga cctctcccg 60  
cctgctcggt cgctctccag cttggg atg gcc ggc tac ctg cgg gtc gtg cgc 113  
Met Ala Gly Tyr Leu Arg Val Val Arg  
1 5  
tcg ctc tgc aga gcc tca ggc tcg cgg ccg gcc tgg gcg ccg gcg gcc 161  
Ser Leu Cys Arg Ala Ser Gly Ser Arg Pro Ala Trp Ala Pro Ala Ala  
10 15 20 25  
ctg aca gcc ccc acc tcg caa gag cag ccg cgg cgc cac tat gcc gac 209  
Leu Thr Ala Pro Thr Ser Gln Glu Gln Pro Arg Arg His Tyr Ala Asp  
30 35 40  
aaa agg atc aag gtg gcg aag ccc gtg gtg gag atg gat ggt gat gag 257  
Lys Arg Ile Lys Val Ala Lys Pro Val Val Glu Met Asp Gly Asp Glu  
45 50 55  
atg acc cgt att atc tgg cag ttc atc aag gag aag ctc atc ctg ccc 305  
Met Thr Arg Ile Ile Trp Gln Phe Ile Lys Glu Lys Leu Ile Leu Pro  
60 65 70

078-us1.ST25

cac	gtg	gac	atc	cag	cta	aag	tat	ttt	gac	ctc	ggg	ctc	cca	aac	cgt	353
His	Val	Asp	Ile	Gln	Leu	Lys	Tyr	Phe	Asp	Leu	Gly	Leu	Pro	Asn	Arg	
	75					80					85					
gac	cag	act	gat	gac	cag	gtc	acc	att	gac	tct	gca	ctg	gcc	acc	cag	401
Asp	Gln	Thr	Asp	Asp	Gln	Val	Thr	Ile	Asp	Ser	Ala	Leu	Ala	Thr	Gln	
90					95					100					105	
aag	tac	agt	gtg	gct	gtc	aag	tgt	gcc	acc	atc	acc	cct	gat	gag	gcc	449
Lys	Tyr	Ser	Val	Ala	Val	Lys	Cys	Ala	Thr	Ile	Thr	Pro	Asp	Glu	Ala	
				110					115					120		
cgt	gtg	gaa	gag	ttc	aag	ctg	aag	aag	atg	tgg	aaa	agt	ccc	aat	gga	497
Arg	Val	Glu	Glu	Phe	Lys	Leu	Lys	Lys	Met	Trp	Lys	Ser	Pro	Asn	Gly	
			125					130					135			
act	atc	cgg	aac	atc	ctg	ggg	ggg	act	gtc	ttc	cgg	gag	ccc	atc	atc	545
Thr	Ile	Arg	Asn	Ile	Leu	Gly	Gly	Thr	Val	Phe	Arg	Glu	Pro	Ile	Ile	
		140				145						150				
tgc	aaa	aac	atc	cca	cgc	cta	gtc	cct	ggc	tgg	acc	aag	ccc	atc	acc	593
Cys	Lys	Asn	Ile	Pro	Arg	Leu	Val	Pro	Gly	Trp	Thr	Lys	Pro	Ile	Thr	
	155					160					165					
att	ggc	agg	cac	gcc	cat	ggc	gac	cag	tac	aag	gcc	aca	gac	ttt	gtg	641
Ile	Gly	Arg	His	Ala	His	Gly	Asp	Gln	Tyr	Lys	Ala	Thr	Asp	Phe	Val	
170					175					180					185	
gca	gac	cgg	gcc	ggc	act	ttc	aaa	atg	gtc	ttc	acc	cca	aaa	gat	ggc	689
Ala	Asp	Arg	Ala	Gly	Thr	Phe	Lys	Met	Val	Phe	Thr	Pro	Lys	Asp	Gly	
				190					195					200		
agt	ggt	gtc	aag	gag	tgg	gaa	gtg	tac	aac	ttc	ccc	gca	ggc	ggc	gtg	737
Ser	Gly	Val	Lys	Glu	Trp	Glu	Val	Tyr	Asn	Phe	Pro	Ala	Gly	Gly	Val	
			205					210					215			
ggc	atg	ggc	atg	tac	aac	acc	gac	gag	tcc	atc	tca	ggt	ttt	gcg	cac	785
Gly	Met	Gly	Met	Tyr	Asn	Thr	Asp	Glu	Ser	Ile	Ser	Gly	Phe	Ala	His	
		220					225					230				
agc	tgc	ttc	cag	tat	gcc	atc	cag	aag	aaa	tgg	ccg	ctg	tac	atg	agc	833
Ser	Cys	Phe	Gln	Tyr	Ala	Ile	Gln	Lys	Lys	Trp	Pro	Leu	Tyr	Met	Ser	
	235				240						245					
acc	aag	aac	acc	ata	ctg	aaa	gcc	tac	gat	ggg	cgt	ttc	aag	gac	atc	881
Thr	Lys	Asn	Thr	Ile	Leu	Lys	Ala	Tyr	Asp	Gly	Arg	Phe	Lys	Asp	Ile	
250					255					260					265	
ttc	cag	gag	atc	ttt	gac	aag	cac	tat	aag	acc	gac	ttc	gac	aag	aat	929
Phe	Gln	Glu	Ile	Phe	Asp	Lys	His	Tyr	Lys	Thr	Asp	Phe	Asp	Lys	Asn	
				270					275					280		
aag	atc	tgg	tat	gag	cac	cgg	ctc	att	gat	gac	atg	gtg	gct	cag	gtc	977
Lys	Ile	Trp	Tyr	Glu	His	Arg	Leu	Ile	Asp	Asp	Met	Val	Ala	Gln	Val	
			285					290					295			
ctc	aag	tct	tcg	ggt	ggc	ttt	gtg	tgg	gcc	tgc	aag	aac	tat	gac	gga	1025
Leu	Lys	Ser	Ser	Gly	Gly	Phe	Val	Trp	Ala	Cys	Lys	Asn	Tyr	Asp	Gly	
		300					305					310				
gat	gtg	cag	tca	gac	atc	ctg	gcc	cag	ggc	ttt	ggc	tcc	ctt	ggc	ctg	1073

078-us1.ST25

Asp	Val	Gln	Ser	Asp	Ile	Leu	Ala	Gln	Gly	Phe	Gly	Ser	Leu	Gly	Leu	
315						320					325					
atg	acg	tcc	gtc	ctg	gtc	tgc	cct	gat	ggg	aag	acg	att	gag	gct	gag	1121
Met	Thr	Ser	Val	Leu	Val	Cys	Pro	Asp	Gly	Lys	Thr	Ile	Glu	Ala	Glu	
330					335					340					345	
gcc	gct	cat	ggg	acc	gtc	acc	cgc	cac	tat	cgg	gag	cac	cag	aag	ggc	1169
Ala	Ala	His	Gly	Thr	Val	Thr	Arg	His	Tyr	Arg	Glu	His	Gln	Lys	Gly	
				350					355					360		
cgg	ccc	acc	agc	acc	aac	ccc	atc	gcc	agc	atc	ttt	gcc	tgg	aca	cgt	1217
Arg	Pro	Thr	Ser	Thr	Asn	Pro	Ile	Ala	Ser	Ile	Phe	Ala	Trp	Thr	Arg	
			365					370					375			
ggc	ctg	gag	cac	cgg	ggg	aag	ctg	gat	ggg	aac	caa	gac	ctc	atc	agg	1265
Gly	Leu	Glu	His	Arg	Gly	Lys	Leu	Asp	Gly	Asn	Gln	Asp	Leu	Ile	Arg	
		380					385					390				
ttt	gcc	cag	atg	ctg	gag	aag	gtg	tgc	gtg	gag	acg	gtg	gag	agt	gga	1313
Phe	Ala	Gln	Met	Leu	Glu	Lys	Val	Cys	Val	Glu	Thr	Val	Glu	Ser	Gly	
	395					400					405					
gcc	atg	acc	aag	gac	ctg	gcg	ggc	tgc	att	cac	ggc	ctc	agc	aat	gtg	1361
Ala	Met	Thr	Lys	Asp	Leu	Ala	Gly	Cys	Ile	His	Gly	Leu	Ser	Asn	Val	
410					415					420					425	
aag	ctg	aac	gag	cac	ttc	ctg	aac	acc	acg	gac	ttc	ctc	gac	acc	atc	1409
Lys	Leu	Asn	Glu	His	Phe	Leu	Asn	Thr	Thr	Asp	Phe	Leu	Asp	Thr	Ile	
				430					435					440		
aag	agc	aac	ctg	gac	aga	gcc	ctg	ggc	agg	cag	tag	ggggaggcgc				1455
Lys	Ser	Asn	Leu	Asp	Arg	Ala	Leu	Gly	Arg	Gln						
			445					450								
cacccatggc	tg	cagtggag	ggg	ccagggc	tg	agccggcg	gg	tcctcctg	ag	cgcggcag						1515
agggtgagcc	tc	acagcccc	tct	ctggagg	c	tttctagg	gg	atgttttt	tt	tataagcca						1575
gatgttttta	aa	agcatatg	tgt	gtttccc	ct	catggtga	cg	tgaggcag	gag	cagtgcg						1635
ttttacctca	gcc	agtcagt	at	gttttgca	tact	gtaatt	tat	attgccc	tt	ggaacaca						1695
tggtgccata	tt	tagctact	aaaa	agctct	tc	acaaaaaa	aaaa									1740

<210> 4  
 <211> 452  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Met Ala Gly Tyr Leu Arg Val Val Arg Ser Leu Cys Arg Ala Ser Gly  
 1 5 10 15

Ser Arg Pro Ala Trp Ala Pro Ala Ala Leu Thr Ala Pro Thr Ser Gln  
 20 25 30

Glu Gln Pro Arg Arg His Tyr Ala Asp Lys Arg Ile Lys Val Ala Lys  
 35 40 45

078-us1.ST25

Pro Val Val Glu Met Asp Gly Asp Glu Met Thr Arg Ile Ile Trp Gln  
50 55 60

Phe Ile Lys Glu Lys Leu Ile Leu Pro His Val Asp Ile Gln Leu Lys  
65 70 75 80

Tyr Phe Asp Leu Gly Leu Pro Asn Arg Asp Gln Thr Asp Asp Gln Val  
85 90 95

Thr Ile Asp Ser Ala Leu Ala Thr Gln Lys Tyr Ser Val Ala Val Lys  
100 105 110

Cys Ala Thr Ile Thr Pro Asp Glu Ala Arg Val Glu Glu Phe Lys Leu  
115 120 125

Lys Lys Met Trp Lys Ser Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly  
130 135 140

Gly Thr Val Phe Arg Glu Pro Ile Ile Cys Lys Asn Ile Pro Arg Leu  
145 150 155 160

Val Pro Gly Trp Thr Lys Pro Ile Thr Ile Gly Arg His Ala His Gly  
165 170 175

Asp Gln Tyr Lys Ala Thr Asp Phe Val Ala Asp Arg Ala Gly Thr Phe  
180 185 190

Lys Met Val Phe Thr Pro Lys Asp Gly Ser Gly Val Lys Glu Trp Glu  
195 200 205

Val Tyr Asn Phe Pro Ala Gly Gly Val Gly Met Gly Met Tyr Asn Thr  
210 215 220

Asp Glu Ser Ile Ser Gly Phe Ala His Ser Cys Phe Gln Tyr Ala Ile  
225 230 235 240

Gln Lys Lys Trp Pro Leu Tyr Met Ser Thr Lys Asn Thr Ile Leu Lys  
245 250 255

Ala Tyr Asp Gly Arg Phe Lys Asp Ile Phe Gln Glu Ile Phe Asp Lys  
260 265 270

His Tyr Lys Thr Asp Phe Asp Lys Asn Lys Ile Trp Tyr Glu His Arg  
275 280 285

Leu Ile Asp Asp Met Val Ala Gln Val Leu Lys Ser Ser Gly Gly Phe



290

295

Val Trp Ala Cys Lys Asn Tyr Asp Gly Asp Val Gln Ser Asp Ile Leu  
305 310 315 320

Ala Gln Gly Phe Gly Ser Leu Gly Leu Met Thr Ser Val Leu Val Cys  
325 330 335

Pro Asp Gly Lys Thr Ile Glu Ala Glu Ala Ala His Gly Thr Val Thr  
340 345 350

Arg His Tyr Arg Glu His Gln Lys Gly Arg Pro Thr Ser Thr Asn Pro  
355 360 365

Ile Ala Ser Ile Phe Ala Trp Thr Arg Gly Leu Glu His Arg Gly Lys  
370 375 380

Leu Asp Gly Asn Gln Asp Leu Ile Arg Phe Ala Gln Met Leu Glu Lys  
385 390 395 400

Val Cys Val Glu Thr Val Glu Ser Gly Ala Met Thr Lys Asp Leu Ala  
405 410 415

Gly Cys Ile His Gly Leu Ser Asn Val Lys Leu Asn Glu His Phe Leu  
420 425 430

Asn Thr Thr Asp Phe Leu Asp Thr Ile Lys Ser Asn Leu Asp Arg Ala  
435 440 445

Leu Gly Arg Gln  
450

<210> 5  
<211> 531  
<212> DNA  
<213> Homo sapiens

<400> 5  
tgctctgtgg gctaaccctc tgggtccaggc aaaaatggaa gcaatgggat tgggtggacgt 60  
ctcctgtcct ttcttggtaca tgcggttagtg acgggttaca gtcccgtggg cagcctctgc 120  
ttctaccgtc ttgccatctg gacaaaccag cacgctggtc atcatgccga gagagccata 180  
cccttggggc acagagtcgc actgcacgtc accatcatag tttttacagg cccagatgaa 240  
gcctccctct gatctcatag ctggggccac catgtcgtcg atgagcctat gctcatacca 300  
gatcttttga gcttcaaact gggacttgta ctgcttgta tatactctct gaaagatgtc 360  
ttaaaacgc ccatcatatt tcttcagaat ggtgtttttg gtgctcagat acaaaggcca 420

078-us1.ST25  
acccttagac agagccattt ggaaggaact gtgtgcaaaa tcttcaattg acttatcttg 480  
attatacatc cccatgacaa caccaccacc ttcttcaagt tatgtaccag g 531  
  
<210> 6  
<211> 21  
<212> DNA  
<213> Homo sapiens  
  
<400> 6  
aaucgugaug ccaccaacga c 21